OM protein - protein search, using sw model

Copyright (c) 1993 - 2003 Compugen Ltd

GenCore version 5.1.3

Run on: January 16, 2003, 16:34:12 ; Search time 16.0386 Seconds
                                       (without alignments)
                                       28.464 Million cell updates/sec

Title: US-09-856-070-23
Perfect score: 55
Sequence: 1 ELMLRLQDYEE 11

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   SwissProt_40;*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	55	100.0	580	1	EZRI_BOVIN	P31975 bos taurus
2	55	100.0	585	1	EZRI_HUMAN	P15311 homo sapien
3	52	94.5	585	1	EZRI_MOUSE	P26040 mus musculu
4	39	70.9	886	1	RA50_SULAC	O33600 sulfolobus
5	36	65.5	715	1	BBS2_BRARE	Q98sp7 brachydanio
6	36	65.5	2472	1	SPN_HUMAN	Q13813 homo sapien
7	36	65.5	2472	1	SFCN_RAT	P16086 rattus norv
8	36	65.5	2477	1	SPCN_CHICK	P07751 gallus gall
9	35	63.6	892	1	AAC1_HUMAN	P12814 homo sapien
10	35	63.6	892	1	AAC1_RAT	Q9r1p2 rattus norv
11	35	63.6	964	1	PLEI_MOUSE	Q9qxs1 mus musculu
12	35	63.6	4473	1	PLEI_CRIGR	Q9j155 cricetulus
13	35	63.6	4684	1	PLEI_HUMAN	Q15149 homo sapien
14	35	63.6	4687	1	PLEI_PAT	P30427 rattus norv
15	34	61.8	332	1	KC2A_MAIZE	P28523 zea mays (m
16	34	61.8	333	1	KC21_ARATH	Q08467 arabidopsis
17	34	61.8	333	1	KC22_ARATH	Q08466 arabidopsis
18	34	61.8	333	1	KC23_ARATH	Q64817 arabidopsis
19	34	61.8	365	1	ECT1_SCHPO	Q9u116 schizosacch
20	34	61.8	387	1	YCH5_YEAST	P53159 saccharomyc
21	34	61.8	405	1	FUT4_HUMAN	P22083 homo sapien
22	34	61.8	467	1	INVO_MOUSE	P48997 mus musculu
23	34	61.8	544	1	THS_METTL	093624 methanococc
24	34	61.8	741	1	RSC2_TROMF	P11929 drosophila
25	34	61.8	860	1	RA50_PYRAB	Q44408 pyrococcus
26	34	61.8	978	1	RA50_AQUAE	O67124 aquifex aeo
27	33	60.0	177	1	PUR6_CORAM	Q44479 corynebacte
28	33	60.0	196	1	VITA_BPT7	P07476 bacteriopha
29	33	60.0	226	1	YM74_YEAST	P05024 saccharomyc
30	33	60.0	258	1	Y79A_MYCTU	Q10859 mycobacteri
31	33	60.0	270	1	CWFG_SCHPO	Q9p7c5 schizosacch
32	33	60.0	320	1	HIT1_HUMAN	P54257 homo sapien
33	33	60.0	522	1	CFV1_ORENI	P70091 oreochromis
34	33	60.0	548	1	KUCR_MOUSE	P70194 mus musculu
35	33	60.0	622	1	AMT1_CAPT	O21565 caenorhabdi
36	33	60.0	721	1	BBS2_HUMAN	Q9bxc9 homo sapien
37	33	60.0	721	1	BBS2_MOUSE	Q99cw16 mus musculu
38	33	60.0	721	1	BBS2_PAT	Q99mk9 rattus norv
39	33	60.0	822	1	FER_HUMAN	P16591 homo sapien
40	33	60.0	1521	1	EMB5_CAEEL	P34703 caenorhabdi
41	32.5	59.1	554	1	CSF1_HUMAN	P09603 homo sapien
42	32	58.2	289	1	SQV3_CAEEL	P34548 caenorhabdi
43	32	58.2	303	1	CHEV_BACSU	P17599 bacillus su
44	32	58.2	385	1	SYW_PYRAB	Q9uy11 pyrococcus
45	32	58.2	404	1	EX7L_FUSNN	Q8tcn3 fusobacteri

ALIGNMENTS

RESULT 1
EZRI_BOVIN
ID   EZRI_BOVIN   STANDARD;   PRT;   580 AA.
AC   P31976;
DT   01-JUL-1993 (Rel. 26, Created)
DT   01-JUL-1993 (Rel. 26, Last sequence update)
DT   15-OCT-2001 (Rel. 40, Last annotation update)
DE   Ezrin (p81) (Cytovillin) (Villin 2).
GN   VIL2.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Bergson C.M., Zhao H., Saijoh K., Duman P.S.;
RT   "Ezrin and osteonectin, two proteins associated with cell shape and
RT   growth, are enriched in the locus coeruleus.";
RL   Mol. Cell. Neurosci. 4:64-73(1993).
RN   [2]
RP   SEQUENCE OF 1-15 AND 126-140.
RC   TISSUE=Kidney;
RX   MEDLINE=96239137; PubMed=8660651;
RA   Calat A., Gotbud M.C., Bouet F., Riviere S.;
RT   "Proteins and their amino acid compositions: uniqueness, variability,
RT   and applications.";
RL   Arch. Biochem. Biophys. 330:229-237(1996).
CC   -!- FUNCTION: PROBABLY INVOLVED IN CONNECTIONS OF MAJOR CYTOSKELETAL
CC   STRUCTURES TO THE PLASMA MEMBRANE.
CC   -!- SUBCELLULAR LOCATION: MICROVILLAR PERIPHERAL MEMBRANE PROTEIN
CC   (CYTOPLASMIC SIDE).
CC   -!- PTM: PHOSPHORYLATED BY PROTEIN-TYROSINE KINASES.
CC   -!- SIMILARITY: CONTAINS 1 BAND 4.1-LIKE DOMAIN.
CC   --
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed usage by and for commercial
CC   entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --
DR   EMBL; M98498; AAA30510.1; -.
DR   InterPro; IPR000299; Band_4.1.
DR   InterPro; IPR000798; EZ/radixin/moesin.
DR   Pfam; PF00373; Band_41; 1.
DR   Pfam; PF00769; ERM; 1.
DR   PRINTS; PR00935; HAND41.
DR   SMART; SM00295; B41; 1.
DR   PROSITE; PS00660; BAND_41_1; 1.
DR   PROSITE; PS00661; BAND_41_2; 1.
DR   PROSITE; PS50057; BAND_41_3; 1.
KW   Structural protein; Cytoskeleton; Phosphorylation.
FT   INIT_MET   0   0

```
FT   DOMAIN        57    224        BAND 4.1-LIKE.
FT   MOD_RES      145    145        PHOSPHORYLATION (BY PDGFR)
FT                                  (BY SIMILARITY).
FT   MOD_RES      353    353        PHOSPHORYLATION (BY PDGFR)
FT                                  (BY SIMILARITY).
SQ   SEQUENCE    580 AA;  68629 MW;  E0D663E5C260FAA3 CRC64;

Query Match             100.0%;  Score 55;  DB 1;  Length 580;
Best Local Similarity   100.0%;  Pred. No. 0.005;
Matches    11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1  ELMLRLQDYEE 11
           |||||||||||
Db    345  ELMLRLQDYEE 355

RESULT 2
EZRI_HUMAN
ID   EZRI_HUMAN      STANDARD;        PRT;    585 AA.
AC   P15311; P21714; Q9NSJ4;
DT   01-APR-1990 (Rel. 14, Created)
DT   01-NOV-1991 (Rel. 20, last sequence update)
DT   15-JUN-2002 (Rel. 41, last annotation update)
DE   Ezrin (p81) (Cytovillin) (Villin 2).
GN   VIL2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
RX   MEDLINE=90076135; PubMed=2591371;
RA   Gould K.L., Bretscher A., Esch F.S., Hunter T.;
RT   "cDNA cloning and sequencing of the protein-tyrosine kinase
RT   substrate ezrin reveals homology to band 4.1.";
RL   EMBO J. 8:4133-4142(1989).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RX   MEDLINE=89380299; PubMed=2674140;
RA   Turunen O., Winqvist R., Pakkanen R., Grzeschik K.-H., Wahlstrom T.,
RA   Vaheri A.;
RT   "Cytovillin, a microvillar Mr 75,000 protein. cDNA sequence,
RT   prokaryotic expression, and chromosomal localization.";
RL   J. Biol. Chem. 264:16727-16732(1989).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Ottenwaelder B., Obermaier B., Mewes H.-W., Weil B., Wiemann S.;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE OF 171-179 AND 342-349.
RX   MEDLINE=96311348; PubMed=8711105;
RA   Egerton M., Moritz R.L., Druker B., Kelso A., Simpson R.J.;
RT   "Identification of the 70kD heat shock cognate protein (Hsc70) and
RT   alpha actinin 1 as novel phosphotyrosine-containing proteins in T
RT   lymphocytes.";
RL   Biochem. Biophys. Res. Commun. 224:666-674(1996).
RN   [5]
RP   PHOSPHORYLATION BY PDGFR
RX   MEDLINE=92406868; PubMed=1382070;
RA   Krieg J., Hunter T.;
RT   "Identification of the two major epidermal growth factor-induced
RT   tyrosine phosphorylation sites in the microvillar core protein
RT   ezrin.";
RL   J. Biol. Chem. 267:19258-19265(1992).
RN   [6]
RP   PHOSPHORYLATION.
RX   MEDLINE=92406849; PubMed=1381489;
RA   Egerton M., Burgess W.H., Chen D., Druker B.J., Bretscher A.,
RA   Samelson L.E.;
RT   "Identification of ezrin as an 81 kDa tyrosine-phosphorylated protein
RT   in T cells.";
RL   J. Immunol. 149:1847-1852(1992).

CC   -!- FUNCTION: PROBABLY INVOLVED IN CONNECTIONS OF MAJOR CYTOSKELETAL
CC       STRUCTURES TO THE PLASMA MEMBRANE.
CC   -!- SUBCELLULAR LOCATION: MICROVILLAR PERIPHERAL MEMBRANE PROTEIN
CC       (CYTOPLASMIC SIDE).
CC   -!- TISSUE SPECIFICITY: COMPONENT OF THE MICROVILLI OF INTESTINAL
CC       EPITHELIAL CELLS.
CC   -!- PTM: PHOSPHORYLATED BY PROTEIN-TYROSINE KINASES.
CC   -!- SIMILARITY: CONTAINS 1 BAND 4.1-LIKE DOMAIN.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; X51521; CAA35893.1; -.
DR   EMBL; J05021; AAA61278.1; ALT_INIT.
DR   EMBL; AL162086; CAB82418.1; ALT_INIT.
DR   PIR; S09263; S09263.
DR   PIR; A34400; A34400.
DR   SWISS-2DPAGE; P15311; HUMAN.
DR   Genew; HGNC:12691; VIL2.
DR   MIM; 123900; -.
DR   InterPro; IPR000299; Band_4.1.
DR   InterPro; IPR008746; F/ezr/moesin.
DR   Pfam; PF00373; Band_41; 1.
DR   Pfam; PF00769; ERM; 1.
DR   PRINTS; PR00935; BAND41.
DR   SMART; SM00295; B41; 1.
DR   PROSITE; PS00660; BAND_41_1; 1.
DR   PROSITE; PS00661; BAND_41_2; 1.
DR   PROSITE; PS50057; BAND_41_3; 1.
KW   Structural protein; Cytoskeleton; Phosphorylation.
FT   INIT_MET      0      0
FT   DOMAIN       57    224        BAND 4.1-LIKE.
FT   MOD_RES     145    145        PHOSPHORYLATION (BY PDGFR).
FT   MOD_RES     353    353        PHOSPHORYLATION (BY PDGFR).
FT   CONFLICT    531    531        V -> L. (IN REF. 3).
SQ   SEQUENCE    585 AA;  69267 MW;  2A844D140E3B06CC CRC64;

Query Match             100.0%;  Score 55;  DB 1;  Length 585;
Best Local Similarity   100.0%;  Pred. No. 0.0051;
Matches    11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1  ELMLRLQDYEE 11
           |||||||||||
Db    345  ELMLRLQDYEE 355

RESULT 3
EZRI_MOUSE
ID   EZRI_MOUSE      STANDARD;        PRT;    585 AA.
AC   P26040;
DT   01-MAY-1992 (Rel. 22, Created)
DT   01-MAY-1992 (Rel. 22, last sequence update)
DT   16-OCT-2001 (Rel. 40, last annotation update)
DE   Ezrin (p81) (Cytovillin) (Villin 2).
GN   VIL2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92064635; PubMed-1955455;
RA   Funayama N., Nagafuchi A., Sato N., Tsukita S., Tsukita S.;
RT   "Radixin is a novel member of the band 4.1 family.";
RL   J. Cell Biol. 115:1039-1048(1991).
CC   -!- FUNCTION: PROBABLY INVOLVED IN CONNECTIONS OF MAJOR CYTOSKELETAL
CC       STRUCTURES TO THE PLASMA MEMBRANE.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic.
```

CC   -!- TISSUE SPECIFICITY: COMPONENT OF THE MICROVILLI OF INTESTINAL
CC   EPITHELIAL CELLS.
CC   -!- PIM: PHOSPHORYLATED BY PROTEIN-TYROSINE KINASES.
CC   -!- SIMILARITY: CONTAINS 1 BAND 4.1-LIKE DOMAIN.
CC   --
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --
DR   EMBL; X60671; CAA43086.1; -.
DR   PIR; B41129; B41129.
DR   MGD; MGI:98931; Vil2.
DR   InterPro; IPR000299; Band_4_1.
DR   InterPro; IPR000798; Ez/rad/moesin.
DR   Pfam; PF00373; Band_41; 1.
DR   Pfam; PF00769; ERM; 1.
DR   PRINTS; PR00935; BAND41.
DR   SMART; SM00295; B41; 1.
DR   PROSITE; PS00660; BAND_41_1; 1.
DR   PROSITE; PS00661; BAND_41_2; 1.
DR   PROSITE; PS00057; BAND_41_3; 1.
KW   Structural protein; Cytoskeleton; Phosphorylation.
FT   INIT_MET   0   0   BY SIMILARITY.
FT   DOMAIN   57   224   BAND 4.1-LIKE.
FT   MOD_RES   145   145   PHOSPHORYLATION (BY PTGFR)
FT   (BY SIMILARITY).
FT   MOD_RES   353   353   PHOSPHORYLATION (BY PTGFR)
FT   (BY SIMILARITY).
SQ   SEQUENCE   585 AA; 69234 MW; 205/EDE2E2B0952C CRC64;

Query Match   94.5%; Score 52; DB 1; Length 585;
Best Local Similarity   90.9%; Pred No 019;
Matches   10, Conservative   1, Mismatches   0, Indels   0, Gaps   0;

Qy   1 ELMLRLQDYEE 11
          |||||||:|||
Db   345 ELMLRLQDYEQ 355

RESULT 4
PA50_SULAC
ID   PA50_SULAC   STANDARD;   PRT;   886 AA.
AC   O33600;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   DNA double-strand break repair rad50 ATPase.
GN   RAD50
OS   Sulfolobus acidocaldarius.
OC   Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC   Sulfolobus.
OX   NCBI_TaxID=2285;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN ATCC 33909 / NCIB 11770 / DSM 639.
RX   MEDLINE=97362314; PubMed=9217174;
RA   Elie C., Baucher M.F., Fondrat C., Forterre P.;
RT   "A protein related to eucaryal and bacterial DNA-motor proteins in the
RT   hyperthermophilic archaeon Sulfolobus acidocaldarius.";
RL   J. Mol. Evol. 45:107-114(1997).
CC   -!- FUNCTION: Involved in DNA double-strand break repair (DSBR). The
CC   rad50/mre11 complex possesses single strand endonuclease activity
CC   and Atf dependent double strand specific exonuclease activity.
CC   Rad50 provides an ATP-dependent control of mre11 by unwinding
CC   and/or repositioning DNA ends into the mre11 active site (By
CC   similarity).
CC   -!- SUBUNIT: Forms a complex with mre11 (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE SMC FAMILY. RAD50 SUBFAMILY.

CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --
DR   EMBL; Y10687; CAA71688.1; -.
DR   InterPro; IPR003439; ABC_transporter.
DR   InterPro; IPR003593; SMC_N.
DR   Pfam; PF02463; SMC_N; 1.
DR   ProDom; PD000006; ABC_transporter; 1
KW   DNA repair; Hydrolase; ATP-binding; Coiled coil.
FT   NP_BIND   30   37   ATP (BY SIMILARITY).
FT   DOMAIN   174   727   COILED COIL (POTENTIAL).
SQ   SEQUENCE   886 AA; 104457 MW; B4A8AE140519A104 CRC64;

Query Match   70.9%; Score 39; DB 1; Length 886;
Best Local Similarity   63.6%; Pred. No. 10;
Matches   7, Conservative   4, Mismatches   4, Indels   1, Gaps   0;

Qy   1 ELMLRLQDYEE 11
          |:||||:|||
Db   259 EIALRLKDFEE 269

RESULT 5
BBS2_BRARE
ID   BBS2_BRARE   STANDARD;   PRT;   715 AA.
AC   Q98SP7;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Bardet Biedl syndrome 2 protein homolog.
GN   BBS2.
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21187310; PubMed=11285252;
RA   Nishimura D.Y., Searby C.C., Carmi R., Elbedour K., Van Maldergem L.,
RA   Fulton A.B., Lam B.L., Powell B.R., Swiderski R.E., Bugge K.E.,
RA   Haider N.B., Kwitek-Black A.E., Ying L., Duhl D.M., Gorman S.M.,
RA   Heon E., Iannaccone A., Bonneau D., Biesecker L.G., Jacobson S.G.,
RA   Stone E.M., Sheffield V.C.;
RT   "Positional cloning of a novel gene on chromosome 16q causing
RT   Bardet-Biedl syndrome (BBS2).";
RL   Hum. Mol. Genet. 10:865-874(2001).
CC   --
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --
DR   EMBL; AF342739; AAK28555.1; -.
SQ   SEQUENCE   715 AA; 79135 MW; 326770A74592C956 CRC64;

Query Match   65.5%; Score 36; DB 1; Length 715;
Best Local Similarity   70.0%; Pred. No. 30;
Matches   7, Conservative   2, Mismatches   2, Indels   0, Gaps   0;

Qy   2 LMLRLQDYEE 11
          ||||:||:||
Db   348 LMLELRNYEE 357

```
RESULT 6
SPCN_HUMAN
ID   SPCN_HUMAN   STANDARD;   PRT;   2472 AA.
AC   Q13813; Q16606; Q9P0V0; Q14186;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Spectrin alpha chain, brain (Spectrin, non-erythroid alpha chain)
DE   (Alpha-II spectrin) (Fodrin alpha chain).
GN   SPTAN1 OR SPTA2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90170948; PubMed=2307671;
RA   Moon R.T., McMahon A.P.;
RT   "Generation of diversity in nonerythroid spectrins. Multiple
RT   polypeptides are predicted by sequence analysis of cDNAs encompassing
RT   the coding region of human nonerythroid alpha-spectrin.";
RL   J. Biol. Chem. 265:4427-4433(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Fetal brain;
RA   Cianci C.D., Morrow J.S.;
RT   "Complete cDNA sequence of human alpha II fetal brain spectrin.";
RL   Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE OF 676-1595 FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=88083942; PubMed=3691949;
RA   McMahon A.P., Moon R.T.;
RT   "Structure and evolution of a non-erythroid spectrin, human
RT   alpha fodrin.";
RL   Biochem. Soc. Trans. 15:804-807(1987).
RN   [4]
RP   SEQUENCE OF 676-1595 FROM N.A.
RX   MEDLINE=87277023; PubMed=3038643;
RA   McMahon A.P., Giebelhaus D.H., Champion J.E., Bailes J.A., Lacey S.,
RA   Carritt B., Henchman S.K., Moon R.T.;
RT   "cDNA cloning, sequencing and chromosome mapping of a non-erythroid
RT   spectrin, human alpha-fodrin.";
RL   Differentiation 34:68-78(1987).
RN   [5]
RP   ERRATUM.
RA   McMahon A.P., Giebelhaus D.H., Champion J.E., Bailes J.A., Lacey S.,
RA   Carritt B., Henchman S.K., Moon R.T.;
RL   Differentiation 34:241-241(1987).
RN   [6]
RP   SEQUENCE OF 811-1529 FROM N.A., VARIANT ILE-1300, AND MUTAGENESIS.
RC   TISSUE=Fetal brain;
RX   MEDLINE=97146462; PubMed=8993318;
RA   Stabach P.R., Cianci C.D., Glantz S.B., Zhang Z., Morrow J.S.;
RT   "Site-directed mutagenesis of alpha II spectrin at codon 1175
RT   modulates its mu-calpain susceptibility.";
RL   Biochemistry 46:57-65(1997).
RN   [7]
RP   SEQUENCE OF 1073-1344 FROM N.A.
RA   Murakami N., Speed W.C., Seaman M.I., Zychowski P.I., Wetterberg L.,
RA   Pakstis A.J., Kidd J.R., Kidd K.K.;
RT   "Association and linkage analyses of the nonerythroid alpha-spectrin
RT   (SPTAN1) gene on chromosome 9q34 with a large Swedish kindred.";
RL   Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: FODRIN, WHICH SEEMS TO BE INVOLVED IN SECRETION,
CC       INTERACTS WITH CALMODULIN IN A CALCIUM-DEPENDENT MANNER AND IS
CC       THIS CANDIDATE FOR THE CALCIUM-DEPENDENT MOVEMENT OF THE
CC       CYTOSKELETON AT THE MEMBRANE.
CC   -!- SUBUNIT: LIKE ERYTHROCYTE SPECTRIN, THE SPECTRIN-LIKE PROTEINS
CC       ARE CAPABLE TO FORM DIMERS WHICH CAN FURTHER ASSOCIATE TO
CC       TETRAMERS.
CC   -!- SIMILARITY: BELONGS TO THE SPECTRIN FAMILY.
CC   -!- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM BINDING DOMAINS.
CC   -!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
CC   -!- SIMILARITY: CONTAINS 23 SPECTRIN REPEATS.
CC   -----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------------
DR   EMBL; J05243; AAA51790.1; -.
DR   EMBL; U83867; AAB41498.1; -.
DR   EMBL; M24773; AAA52468.1; -.
DR   EMBL; M18627; AAA51702.1; -.
DR   EMBL; U26396; AAB60364.1; -.
DR   EMBL; AF148808; AAF26672.1; -.
DR   HSSP; P07751; 1AEY.
DR   Genew; HGNC=11273; SPTAN1.
DR   MIM; 182810; -.
DR   InterPro; IPR002048; EF-hand.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR002017; Spectrin.
DR   Pfam; PF00018; SH3; 1.
DR   Pfam; PF00036; efhand; 4.
DR   Pfam; PF00435; spectrin; 32.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   ProDom; PD000012; EF-hand; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00054; EFh; 2.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00150; SPEC; 20.
DR   PROSITE; PS00018; EF_HAND; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   Cytoskeleton; Membrane; Calmodulin binding; Actin-binding;
KW   Capping protein; Calcium-binding; Repeat; SH3 domain; Polymorphism.
FT   DOMAIN        10     42       SPECTRIN 1.
FT   REPEAT        44    147       SPECTRIN 2.
FT   REPEAT       149    253       SPECTRIN 3.
FT   REPEAT       255    359       SPECTRIN 4.
FT   REPEAT       361    465       SPECTRIN 5.
FT   REPEAT       467    571       SPECTRIN 6.
FT   REPEAT       573    676       SPECTRIN 7.
FT   REPEAT       678    782       SPECTRIN 8.
FT   REPEAT       784    888       SPECTRIN 9.
FT   REPEAT       890    955       SPECTRIN 10.
FT   DOMAIN       967   1026       SH3.
FT   REPEAT      1062   1089       SPECTRIN 11.
FT   REPEAT      1091   1161       SPECTRIN 12.
FT   REPEAT      1208   1231       SPECTRIN 13.
FT   REPEAT      1233   1337       SPECTRIN 14.
FT   REPEAT      1339   1443       SPECTRIN 15.
FT   REPEAT      1445   1549       SPECTRIN 16.
FT   REPEAT      1551   1656       SPECTRIN 17.
FT   REPEAT      1658   1762       SPECTRIN 18.
FT   REPEAT      1764   1868       SPECTRIN 19.
FT   REPEAT      1870   1974       SPECTRIN 20.
FT   REPEAT      1976   2081       SPECTRIN 21.
FT   REPEAT      2091   2195       SPECTRIN 22.
FT   REPEAT      2205   2310       SPECTRIN 23.
FT   CA_BIND     2336   2347       EF-HAND 1 (POTENTIAL).
FT   CA_BIND     2379   2390       EF-HAND 2 (POTENTIAL).
FT   SITE        1176   1177       CLEAVAGE (BY MU-CALPAIN).
FT   VARIANT     1300   1300       I -> T.
FT                                 /FTId=VAR_012227.
FT   CONFLICT     150    150       N -> K (IN REF. 2).
FT   CONFLICT     498    498       F -> S (IN REF. 2).
FT   CONFLICT     737    737       V -> I (IN REF. 2).
FT   CONFLICT    1586   1586       Q -> Q(SKL) (IN REF. 2).
FT   CONFLICT    1595   1595       F -> R (IN REF. 3 AND 4).
FT   CONFLICT    1625   1625       N -> S (IN REF. 2).
FT   CONFLICT    1670   1671       IA -> FD (IN REF. 2).
FT   CONFLICT    1918   1918       A -> D (IN REF. 2).
```

```
FT   CONFLICT    2347   2347    DG -> EF (IN REF. 2).
FT   CONFLICT    2448   2448    I -> Y (IN REF. 2).
SQ   SEQUENCE    2472 AA;  284279 MW; C9A19F44C2A70289 CRC64.

Query Match
Best Local Similarity    65.5%;   Score 36;  DB 1;  Length 2472;
                         63.6%;   Pred No. 1.2e-02;
Matches    7;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy     1 ELMLRLQDYEE 11
         |||||||||
Db   970 ELVLALYDYQE 980

RESULT 7
SPCN_RAT
ID   SPCN_RAT    STANDARD;    PRT;   2472 AA.
AC   P16086; P70477; O88663;
DT   01-APR-1990 (Rel. 14, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Spectrin alpha chain, brain (Spectrin, non-erythroid alpha chain)
DE   (Alpha-II spectrin) (Fodrin alpha chain).
GN   SPTAN1 OR SPTA2.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Wistar; TISSUE=Liver;
RA   Kalamaraki P., Gazzotti P.;
RT   "Structural and functional characterization of the calmodulin and
RT   calpain binding domains of rat liver alpha-II spectrin.";
RL   Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Skeletal muscle;
RA   Zhou D., Ursitti J.A., Porter N.C., Randall W.P., Bloch R.T.;
RT   "Expressional cloning of alpha-fodrin from rat skeletal muscle.";
RL   Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE OF 1292-2321 FROM N.A.
RC   TISSUE=Kidney;
RX   MEDLINE=89327227; PubMed=2753883;
RA   Hong W., Doyle D.;
RT   "Cloning and analysis of cDNA clones for rat kidney alpha-spectrin.";
RL   J. Biol. Chem. 264:12758-12764(1989).
CC   -!- FUNCTION: FODRIN, WHICH SEEMS TO BE INVOLVED IN SECRETION,
CC       INTERACTS WITH CALMODULIN IN A CALCIUM-DEPENDENT MANNER AND IS
CC       THUS CANDIDATE FOR THE CALCIUM-DEPENDENT MOVEMENT OF THE
CC       CYTOSKELETON AT THE MEMBRANE (By similarity).
CC   -!- SUBUNIT: LIKE ERYTHROCYTE SPECTRIN, THE SPECTRIN-LIKE PROTEINS
CC       ARE CAPABLE TO FORM DIMERS WHICH CAN FURTHER ASSOCIATE TO
CC       TETRAMERS.
CC   -!- SIMILARITY: BELONGS TO THE SPECTRIN FAMILY.
CC   -!- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
CC   -!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
CC   -!- SIMILARITY: CONTAINS 23 SPECTRIN REPEATS
CC   -----------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------------------
DR   EMBL; X90845; CAA62350.1; -.
DR   EMBL; AF084186; AAC33127.1; -.
DR   EMBL; J04828; AAA40770.1; -.
DR   PIR; A32612; A32612.
DR   HSSP; P07751; 1AJ3.
DR   InterPro; IPR002048; EF-hand
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR002017; Spectrin.
DR   Pfam; PF00018; SH3; 1.
DR   Pfam; PF00036; efhand; 2.
DR   Pfam; PF00435; spectrin; 33.
DR   SMART; SM00054; EF; 2.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00150; SPEC; 29.
DR   PROSITE; PS00018; EF_HAND; 2.
DR   PROSITE; PS50002; SH3; 1.
KW   Cytoskeleton; Membrane; Calmodulin-binding; Actin-binding;
KW   Capping protein; Calcium-binding; Repeat; SH3 domain.
FT   REPEAT       10     42    SPECTRIN 1.
FT   REPEAT       44    147    SPECTRIN 2.
FT   REPEAT      149    253    SPECTRIN 3.
FT   REPEAT      255    359    SPECTRIN 4.
FT   REPEAT      361    465    SPECTRIN 5.
FT   REPEAT      467    571    SPECTRIN 6.
FT   REPEAT      573    676    SPECTRIN 7.
FT   REPEAT      678    782    SPECTRIN 8.
FT   REPEAT      784    888    SPECTRIN 9.
FT   REPEAT      890    955    SPECTRIN 10.
FT   DOMAIN      967   1026    SH3.
FT   REPEAT     1062   1089    SPECTRIN 11.
FT   REPEAT     1091   1161    SPECTRIN 12.
FT   REPEAT     1208   1231    SPECTRIN 13.
FT   REPEAT     1233   1337    SPECTRIN 14.
FT   REPEAT     1339   1443    SPECTRIN 15.
FT   REPEAT     1445   1549    SPECTRIN 16.
FT   REPEAT     1551   1656    SPECTRIN 17.
FT   REPEAT     1658   1762    SPECTRIN 18.
FT   REPEAT     1764   1868    SPECTRIN 19.
FT   REPEAT     1870   1974    SPECTRIN 20.
FT   REPEAT      ...    ...    SPECTRIN 21.
FT   REPEAT     2091   2195    SPECTRIN 22.
FT   REPEAT     2205   2310    SPECTRIN 23.
FT   CA_BIND    2336   2347    EF-HAND 1 (POTENTIAL).
FT   CA_BIND    2379   2390    EF-HAND 2 (POTENTIAL).
FT   CONFLICT   1329   1329    D -> Y (IN REF. 3).
FT   CONFLICT   1514   1514    V -> L (IN REF. 1).
FT   CONFLICT   1702   1702    V -> A (IN REF. 3).
FT   CONFLICT   1971   1972    KL -> NV (IN REF. 1).
FT   CONFLICT   2205   2206    KL -> NV (IN REF. 1).
FT   CONFLICT   2318   2321    GGQARNTGVT -> IIADPGGEHRSH (IN REF. 3).
SQ   SEQUENCE   2472 AA;  284635 MW; UBDDF01A28712/8A CRC64.

Query Match
Best Local Similarity    65.5%;   Score 36;  DB 1;  Length 2472;
                         63.6%;   Pred No. 1.2e-02;
Matches    7;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy     1 ELMLRLQDYEE 11
         |||||||||
Db   970 ELVLALYDYQE 980

RESULT 8
SPCN_CHICK
ID   SPCN_CHICK    STANDARD;    PRT;   2477 AA.
AC   P07751;
DT   01-AUG-1988 (Rel. 08, Created)
DT   01-AUG-1991 (Rel. 19, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Spectrin alpha chain, brain (Spectrin, non erythroid alpha chain)
DE   (Fodrin alpha chain).
GN   SPTAN1 OR SPTA2.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
PX   MEDLINE=89092238; PubMed=2610979;
```

RA   Waserius V.-M., Saraste M., Salven P., Eraemaa M., Holm M.,
RA   Lehto V.-P.;
RT   "Primary structure of the brain alpha-spectrin.";
RL   J. Cell Biol. 108:79-93(1989).
RN   [2]
RP   REVISIONS.
RA   Waserius V.-M., Saraste M., Salven P., Eraemaa M., Holm L.,
RA   Lehto V.-P.;
RL   J. Cell Biol. 108:1177-1178(1989).
RN   [3]
RP   SEQUENCE OF 1695-2153 FROM N.A.
RX   MEDLINE=85284928; PubMed 4029118;
RA   Waserius V.-M., Saraste M., Knowles J., Virtanen I., Lehto V.-P.;
RT   "Sequencing of the chicken non-erythroid spectrin cDNA reveals an
RT   internal repetitive structure homologous to the human erythrocyte
RT   spectrin.";
RL   EMBO J. 4:1425-1430(1985).
RN   [4]
RP   X-RAY CRYSTALLOGRAPHY (1 A ANGSTROMS) OF 965-1025.
RX   MEDLINE=94063299; PubMed-1279444;
RA   Musacchio A., Noble M., Pauptit R., Wierenga R., Saraste M.;
RT   "Crystal structure of a Src-homology 3 (SH3) domain.";
RL   Nature 359:851-855(1992).
RN   [5]
RP   X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 969-1025.
RX   MEDLINE=98363217; PubMed-9699637;
RA   Martinez J.C., Pisabarro M.T., Serrano L.;
RT   "Obligatory steps in protein folding and the conformational diversity
RT   of the transition state.";
RL   Nat. Struct. Biol. 5:721-729(1998)
RN   [6]
RP   STRUCTURE BY NMR OF 1763-1872.
RX   MEDLINE=98022917; PubMed-9356261;
RA   Pascual J., Pfuhl M., Walther D., Saraste M., Nilges M.;
RT   "Solution structure of the spectrin repeat: a left-handed
RT   antiparallel triple-helical coiled-coil.";
RL   J. Mol. Biol. 273:740-751(1997).
RN   [7]
RP   STRUCTURE BY NMR OF 2320-2403.
RX   MEDLINE=96067121; PubMed-7588621;
RA   Trave G., Lacombe J.-P., Pfuhl M., Saraste M., Pastore A.;
RT   "Molecular mechanism of the calcium-induced conformational change in
RT   the spectrin EF-hands.";
RL   EMBO J. 14:4922-4931(1995).
CC   -!- FUNCTION: MORPHOLOGICALLY, SPECTRIN-LIKE PROTEINS APPEAR TO BE
CC   RELATED TO SPECTRIN, SHOWING A FLEXIBLE ROD-LIKE STRUCTURE.
CC   THEY CAN BIND ACTIN BUT SEEM TO DIFFER IN THEIR CALMODULIN-
CC   BINDING ACTIVITY. IN NONERYTHROID TISSUES, SPECTRINS, IN
CC   ASSOCIATION WITH SOME OTHER PROTEINS, MAY PLAY AN IMPORTANT
CC   ROLE IN MEMBRANE ORGANIZATION
CC   -!- SUBUNIT: LIKE ERYTHROCYTE SPECTRIN, THE SPECTRIN-LIKE PROTEINS
CC   ARE CAPABLE TO FORM DIMERS WHICH CAN FURTHER ASSOCIATE TO
CC   TETRAMERS.
CC   -!- DOMAIN: SPECTRIN-LIKE PROTEINS HAVE FIVE DOMAINS:
CC   (1) N-TERMINAL DOMAIN (N),
CC   (2) DOMAIN BETWEEN THE N-TERMINAL AND MIDDLE DOMAIN (NM),
CC   (3) MIDDLE DOMAIN (M),
CC   (4) DOMAIN BETWEEN THE MIDDLE AND C-TERMINAL DOMAIN (MC),
CC   (5) C-TERMINAL DOMAIN (C).
CC   NM AND MC DOMAINS ARE COMPOSED OF TYPICAL SPECTRIN 106 RESIDUES
CC   REPEATS (1-8 FOR NM AND 12-19 FOR MC) AND ARE HOMOLOGOUS TO EACH
CC   OTHER. N, M, AND C DOMAINS ARE COMPOSED OF SEQUENCES THAT DO NOT
CC   FORM TYPICAL SPECTRIN REPEATS.
CC   -!- SIMILARITY: BELONGS TO THE SPECTRIN FAMILY.
CC   -!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.

CC   --
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).

DR   EMBL; X14518; CAA32662.1; -.
DR   EMBL; X14519; CAA32663.1; ALT_SEQ.
DR   EMBL; X02593; CAA51571.1; ALT_SEQ.
DR   PIR; A30122; SJCHA.
DR   PDB; 1SHG; 31-OCT-93.
DR   PDB; 1AEY; 15-MAY-97.
DR   PDB; 1AJ3; 07-JUL-97.
DR   PDB; 1TUC; 01-AUG-96.
DR   PDB; 1TUD; 01-AUG-96.
DR   PDB; 1HK2; 16-FEB-99.
DR   InterPro; IPR002048; EF-hand.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR002017; Spectrin.
DR   Pfam; PF00018; SH3; 1.
DR   Pfam; PF00036; efhand; 2.
DR   Pfam; PF00435; spectrin; 23.
DR   PRINTS; PR00452; SH3DOMAIN.
DP   ProDom; PD000011; EF-hand; 1.
DP   ProDom; PD000066; SH3; 1.
DR   SMART; SM00054; EFh; 2.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00150; SPEC; 20.
DR   PROSITE; PS00018; EF_HAND; 2.
DR   PROSITE; PS50002; SH3; 1.
KW   Cytoskeleton; Membrane; Calmodulin-binding; Actin-binding;
KW   Capping protein; Calcium-binding; Repeat; SH3 domain; 3D-structure.
FT   DOMAIN   1   14   N-TERMINAL DOMAIN.
FT   REPEAT   15   119   1.
FT   REPEAT   120   225   2.
FT   REPEAT   226   331   3.
FT   REPEAT   332   437   4.
FT   REPEAT   438   543   5.
FT   REPEAT   544   648   6.
FT   REPEAT   649   754   7.
FT   REPEAT   755   860   8.
FT   REPEAT   861   966   9.
FT   DOMAIN   967   1061   MIDDLE DOMAIN.
FT   DOMAIN   967   1026   SH3.
FT   DOMAIN   1062   2256   MC DOMAIN.
FT   REPEAT   1062   1167   11.
FT   REPEAT   1204   1309   12.
FT   REPEAT   1310   1415   13.
FT   REPEAT   1416   1521   14.
FT   REPEAT   1522   1633   15.
FT   REPEAT   1634   1739   16.
FT   REPEAT   1740   1845   17.
FT   REPEAT   1846   1951   18.
FT   REPEAT   1952   2058   19.
FT   REPEAT   2059   2171   20.
FT   REPEAT   2172   2256   21.
FT   DOMAIN   2257   2477   C-TERMINAL DOMAIN.
FT   CA_BIND   2341   2352   EF-HAND 1 (POTENTIAL).
FT   CA_BIND   2384   2395   EF-HAND 2 (POTENTIAL).
FT   STRAND   971   974
FT   STRAND   978   984
FT   TURN   983   985
FT   STRAND   985   985
FT   STRAND   988   988
FT   TURN   990   991
FT   STRAND   993   998
FT   STRAND   1004   1009
FT   TURN   1010   1011
FT   STRAND   1012   1017
FT   HELIX   1018   1020
FT   STRAND   1021   1024
SQ   SEQUENCE   2477 AA; 285361 MW; AD4C876994E6AB49 CRC64;

Query Match   65.5%; Score 46; DB 1; Length 2477;
Best Local Similarity   63.6%; Prod. No. 1.26e32;
Matches   7; Conservative   2; Mismatches   2; Indels   0; Gaps   0;

Qy   1 ELMLRLQDYEE 11

```
Db    970 ELVLALYDYQE 980
           ||||| ||||
          970 ELVLALYDYQE 980

RESULT 9
AAC1_HUMAN
ID   AAC1_HUMAN             STANDARD;      PRT;    892 AA.
AC   P12814;
DT   01-OCT-1989 (Rel. 12, Created)
DT   01-OCT-1989 (Rel. 12, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Alpha-actinin 1 (Alpha-actinin cytoskeletal isoform) (Non-muscle
DE   alpha-actinin 1) (F-actin cross linking protein).
GN   ACTN1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RX   MEDLINE=89385999; PubMed=2780298;
RA   Millake D.B., Blanchard A.D., Patel B., Critchley D.R.;
RT   "The cDNA sequence of a human placental alpha-actinin.";
RL   Nucleic Acids Res. 17:6725-6725(1989).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90274024; PubMed=2349951;
RA   Youssoufian H., McAfee M., Kwiatkowski D.J.;
RT   "Cloning and chromosomal localization of the human cytoskeletal
RT   alpha-actinin gene reveals linkage to the beta-spectrin gene.";
RL   Am. J. Hum. Genet. 47:62-71(1990).
RN   [3]
RP   SEQUENCE OF 297-892 FROM N.A.
RX   MEDLINE=90381709; PubMed=2169343;
RA   Nishiyama M., Ozturk M., Frohlich M., Mafune K-I., Steele G. Jr.,
RA   Wands J.R.;
RT   "Expression of human alpha-actinin in human hepatocellular
RT   carcinoma.";
RL   Cancer Res. 50:6291-6294(1990).
RN   [4]
RP   SEQUENCE OF 134-146.
RX   MEDLINE=96311348; PubMed=8713105;
RA   Egerton M., Moritz R.L., Druker B., Kelso A., Simpson R.J.;
RT   "Identification of the 70kD heat shock cognate protein (Hsc70) and
RT   alpha-actinin-1 as novel phosphotyrosine-containing proteins in T
RT   lymphocytes.";
RL   Biochem. Biophys. Res. Commun. 224:666-674(1996).
CC   -!- FUNCTION: F-ACTIN CROSS-LINKING PROTEIN WHICH IS THOUGHT TO ANCHOR
CC       ACTIN TO A VARIETY OF INTRACELLULAR STRUCTURES. THIS IS A BUNDLING
CC       PROTEIN.
CC   -!- SUBUNIT: HOMODIMER, ANTIPARALLEL.
CC   -!- SIMILARITY: CONTAINS 1 ACTIN-BINDING DOMAIN.
CC   -!- SIMILARITY: CONTAINS 2 CALPONIN-HOMOLOGY (CH) DOMAINS.
CC   -!- SIMILARITY: CONTAINS 2 EF HAND CALCIUM-BINDING DOMAINS.
CC   -!- SIMILARITY: CONTAINS 4 SPECTRIN REPEATS.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; X15804; CAA33803.1; -.
DR   EMBL; M95178; AAA51582.1; -.
DR   EMBL; X55187; CAA38907.1; -.
DR   PIR; S05503; S05503.
DR   HSSP; Q01082; 1HKR.
DR   Genew; HGNC:163; ACTN1.
DR   MIM; 102575;
DR   InterPro; IPR001589; Actbind_actin.
DR   InterPro; IPR001715; Calponin-like.
DR   InterPro; IPR002048; EF-hand.
DR   InterPro; IPR002017; Spectrin.
DR   Pfam; PF00036; efhand; 2.
DR   Pfam; PF00307; CH; 2.
DR   Pfam; PF00435; spectrin; 4.
DR   ProDom; PD000012; EF-hand; 1.
DR   SMART; SM00033; CH; 2.
DR   SMART; SM00054; EFh; 2.
DR   SMART; SM00150; SPEC; 2.
DR   PROSITE; PS00019; ACTININ_1; 1.
DR   PROSITE; PS00020; ACTININ_2; 1.
DR   PROSITE; PS50021; CH; 2.
DR   PROSITE; PS00018; EF_HAND; 1.
KW   Actin-binding; Calcium-binding; Repeat; Multigene family.
FT   DOMAIN       1    247       ACTIN-BINDING.
FT   DOMAIN      31    135       CH 1.
FT   DOMAIN     144    247       CH 2.
FT   REPEAT     274    384       SPECTRIN 1.
FT   REPEAT     394    499       SPECTRIN 2.
FT   REPEAT     509    620       SPECTRIN 3.
FT   REPEAT     630    733       SPECTRIN 4.
FT   CA_BIND    759    770       EF-HAND 1 (POTENTIAL).
FT   CA_BIND    800    811       EF-HAND 2 (POTENTIAL).
FT   CONFLICT   317    317       R -> L (IN REF. 3).
FT   CONFLICT   477    477       Q -> L (IN REF. 3).
FT   CONFLICT   630    631       SV -> RL (IN REF. 3).
FT   CONFLICT   654    654       G -> A (IN REF. 3).
FT   CONFLICT   656    656       I -> F (IN REF. 3).
FT   CONFLICT   674    674       Y -> F (IN REF. 3).
FT   CONFLICT   778    778       L -> S (IN REF. 3).
SQ   SEQUENCE   892 AA;  102974 MW;  2CAFC22FE55AF74 CRC64;

Query Match             63.9%;  Score 35;  DB 1;  Length 892;
Best Local Similarity   70.0%;  Pred. No. 60;
Matches    7;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        1 ELMKLQDYE 10
            | ||| |||
Db      414 EAMLRQKDYE 423

RESULT 10
AAC1_RAT
ID   AAC1_RAT               STANDARD;      PRT;    892 AA.
AC   Q9Z1P2;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-OCT-2001 (Rel. 40, Last annotation update)
DE   Alpha-actinin 1 (Alpha-actinin cytoskeletal isoform) (Non-muscle
DE   alpha-actinin 1) (F-actin cross linking protein).
GN   ACTN1.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Hippocampus;
RA   Schulz T.W., Seeburg P.H.;
RT   "Rattus norvegicus non muscle alpha actinin 1 mRNA.";
RL   Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: F-ACTIN CROSS-LINKING PROTEIN WHICH IS THOUGHT TO ANCHOR
CC       ACTIN TO A VARIETY OF INTRACELLULAR STRUCTURES. THIS IS A BUNDLING
CC       PROTEIN (BY SIMILARITY).
CC   -!- SUBUNIT: HOMODIMER, ANTIPARALLEL (BY SIMILARITY).
CC   -!- SIMILARITY: CONTAINS 1 ACTIN-BINDING DOMAIN.
CC   -!- SIMILARITY: CONTAINS 2 CALPONIN-HOMOLOGY (CH) DOMAINS.
CC   -!- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
CC   -!- SIMILARITY: CONTAINS 4 SPECTRIN REPEATS.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
```

DR   EMBL; AF115386; AAD12064.1; -.
DR   HSSP; Q01082; 1BKR.
DR   InterPro; IPR001589; Actbind_actin.
DR   InterPro; IPR001715; Calponin-like.
DR   InterPro; IPR002048; EF_hand.
DR   InterPro; IPR002017; Spectrin.
DR   Pfam; PF00046; cfhand; 2.
DR   Pfam; PF09407; CH; 2.
DR   Pfam; PF00435; spectrin; 4.
DR   ProDom; PD000012; EF-hand; 1.
DR   SMART; SM00033; CH; 2.
DR   SMART; SM00054; EFh; 2.
DR   SMART; SM00150; SPEC; 2.
DR   PROSITE; PS00019; ACTININ_1; 1.
DR   PROSITE; PS00020; ACTININ_2; 1.
DR   PROSITE; PS50021; CH; 2.
DR   PROSITE; PS00018; EF_HAND; 1.
KW   Actin-binding; Calcium-binding; Repeat; Multigene family.
FT   DOMAIN   1   247   ACTIN-BINDING.
FT   DOMAIN   31   135   CH 1.
FT   DOMAIN   144   247   CH 2.
FT   REPEAT   274   484   SPECTRIN 1.
FT   REPEAT   394   499   SPECTRIN 2.
FT   REPEAT   509   620   SPECTRIN 3.
FT   REPEAT   630   733   SPECTRIN 4.
FT   CA_BIND   759   770   EF-HAND 1 (POTENTIAL).
FT   CA_BIND   800   811   EF-HAND 2 (POTENTIAL).
SQ   SEQUENCE   892 AA; 102959 MW; 236D496D0A84095 CRC64;

Query Match   63.6%; Score 35; DB 1; Length 892;
Best Local Similarity   70.0%; Prod No. 60;
Matches   7; Conservative   1; Mismatches   2; Indels   2; Gaps   0;

Qy   1 ELMLRLQDYE 10
               |||||:|||
Db   414 EAMLRQKDYE 423

RESULT 11
PLEI_MOUSE
ID   PLEI_MOUSE   STANDARD;   PRT;   964 AA.
AC   Q90XS1; Q90XQ8; Q90XQ9; Q90XR0; Q90XR1; Q90XR3; Q90XR3;
AC   Q90XR4; Q90XR5; Q90XR6; Q90XR7; Q90XR8; Q90XR9; Q90XS2;
AC   Q90XS3; Q9CS65;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Plectin 1 (PLTN) (PCN) (Fragment).
GN   PLEC1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY.
RC   TISSUE=Brain, Embryo, Heart, Kidney, Skeletal muscle, and Testis;
RX   MEDLINE=20925755; PubMed=10556294;
RA   Fuchs P., Zorrer M., Reznicek G.A., Spazierer D., Oehler S.,
RA   Castanon M.J., Hauptmann R., Wiche G.;
RT   "Unusual 5' transcript complexity of plectin isoforms: novel tissue-
RT   specific exons modulate actin binding activity.";
RL   Hum. Mol. Genet. 8:2461-2472(1999).
RN   [2]
RP   SEQUENCE OF 181-812 FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Embryo;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA   Arakawa I., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Bottelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C.A., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
CC   -!- FUNCTION: INTERLINKS INTERMEDIATE FILAMENTS WITH MICROTUBULES AND
CC   MICROFILAMENTS AND ANCHORS INTERMEDIATE FILAMENTS TO DESMOSOMES OR
CC   HEMIDESMOSOMES. MAY BE INVOLVED NOT ONLY IN THE CROSSLINKING AND
CC   STABILIZATION OF CYTOSKELETAL INTERMEDIATE FILAMENTS NETWORK, BUT
CC   ALSO IN THE REGULATION OF THEIR DYNAMICS.
CC   -!- SUBUNIT: HOMODIMER OR HOMOTETRAMER (BY SIMILARITY).
CC   -!- ALTERNATIVE PRODUCTS: 16 ISOFORMS: PLEC-1,2A (SHOWN HERE), PLEC-1,
CC   PLEC-1A, PLEC-1B,2A, PLEC-1B, PLEC-0,1C,2A, PLEC-
CC   0,1C,2A,3A, PLEC-1D,2A, PLEC-1D, PLEC-1E,2A, PLEC-1E, PLEC-1F,
CC   PLEC-1G, PLEC-1H AND PLEC-1I, ARE PRODUCED BY ALTERNATIVE
CC   SPLICING.
CC   -!- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN LUNG, BRAIN, SMALL
CC   INTESTINE, MUSCLE, HEART AND SKIN WITH LOWER LEVELS FOUND IN
CC   KIDNEY, LIVER, UTERUS, SPLEEN AND SALIVARY GLAND.
CC   -!- DOMAIN: THE N-TERMINUS INTERACTS WITH ACTIN, THE C-TERMINUS WITH
CC   VIMENTIN, DESMIN, GFAP, CYTOKERATINS, LAMIN B; WHEREAS BOTH THE N-
CC   AND THE C-TERMINUS CAN BIND INTEGRIN BETA-4.
CC   -!- PTM: PHOSPHORYLATED BY CDC2, REGULATES DISSOCIATION FROM
CC   INTERMEDIATE FILAMENTS DURING MITOSIS (BY SIMILARITY).
CC   -!- SIMILARITY: CONTAINS 1 ACTIN-BINDING DOMAIN.
CC   -!- SIMILARITY: CONTAINS 2 CALPONIN-HOMOLOGY (CH) DOMAINS.
CC   -!- SIMILARITY: CONTAINS 3 SPECTRIN REPEATS.
CC   -!- SIMILARITY: BELONGS TO THE PLAKIN OR CYTOLINKER FAMILY.
DR   EMBL; AF188006; AAF18066.1; -.
DR   EMBL; AF188007; AAF18067.1; -.
DR   EMBL; AF188008; AAF18068.1; -.
DR   EMBL; AF188009; AAF18069.1; -.
DR   EMBL; AF188010; AAF18070.1; -.
DR   EMBL; AF188011; AAF18071.1; -.
DR   EMBL; AF188012; AAF18072.1; -.
DR   EMBL; AF188013; AAF18073.1; -.
DR   EMBL; AF188014; AAF18074.1; -.
DR   EMBL; AF188015; AAF18075.1; -.
DR   EMBL; AF188016; AAF18076.1; -.
DR   EMBL; AF188017; AAF18077.1; -.
DR   EMBL; AF188018; AAF18078.1; -.
DR   EMBL; AF188019; AAF18079.1; -.
DR   EMBL; AF188020; AAF18080.1; -.
DR   EMBL; AF188021; AAF18081.1; -.
DR   EMBL; AF188022; AAF18082.1; -.
DR   EMBL; AF188023; AAF18083.1; -.
DR   EMBL; AK017743; BAB30907.1; ALT_INIT.
DR   MGI; 1277961; Plec1.
DR   InterPro; IPR001589; Actbind_actin.
DR   InterPro; IPR001715; Calponin-like.

```
ID   PLEI_CRIGR              STANDARD;      PRT;   4473 AA.
AC   Q9JI55;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Plectin 1 (PLTN) (PCN) (300-kDa intermediate filament-associated
DE   protein) (IFAP300) (Fragment).
GN   PLEC1.
OS   Cricetulus griseus (Chinese hamster).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC   Cricetulus.
OX   NCBI_TaxID=10029;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20334248; PubMed=10873583;
RA   Clubb B.H., Chou Y.-H., Herrmann H., Svitkina T.M., Borisy G.G.,
RA   Goldman R.D.;
RT   "The 300-kDa intermediate filament associated protein (ifAP300) is a
RT   hamster plectin ortholog.";
RL   Biochem. Biophys. Res. Commun. 273:183-187(2000).
RN   [2]
RP   PHOSPHORYLATION.
RX   MEDLINE=96215219; PubMed=8621512;
RA   Malecz N., Foisner R., Stadler C., Wiche G.;
RT   "Identification of plectin as a substrate of p34cdc2 kinase and
RT   mapping of a single phosphorylation site.";
RL   J. Biol. Chem. 271:8203-8208(1996).
CC   -!- FUNCTION: INTERLINKS INTERMEDIATE FILAMENTS WITH MICROTUBULES AND
CC       MICROFILAMENTS AND ANCHORS INTERMEDIATE FILAMENTS TO DESMOSOMES OR
CC       HEMIDESMOSOMES. MAY BE INVOLVED NOT ONLY IN THE CROSSLINKING AND
CC       STABILIZATION OF CYTOSKELETAL INTERMEDIATE FILAMENTS NETWORK, BUT
CC       ALSO IN THE REGULATION OF THEIR DYNAMICS.
CC   -!- SUBUNIT: HOMODIMER OR HOMOTETRAMER.
CC   -!- DOMAIN: THE N-TERMINUS INTERACTS WITH ACTIN, THE C-TERMINUS WITH
CC       VIMENTIN, DESMIN, GFAP, CYTOKERATINS, LAMIN B; WHEREAS BOTH THE N-
CC       AND THE C-TERMINUS CAN BIND INTEGRIN BETA-4.
CC   -!- PTM: PHOSPHORYLATED BY CDC2. REGULATES DISSOCIATION FROM
CC       INTERMEDIATE FILAMENTS DURING MITOSIS.
CC   -!- SIMILARITY: CONTAINS 1 ACTIN-BINDING DOMAIN.
CC   -!- SIMILARITY: CONTAINS 2 CALPONIN-HOMOLOGY (CH) DOMAINS.
CC   -!- SIMILARITY: CONTAINS 32 PLECTIN REPEATS.
CC   -!- SIMILARITY: CONTAINS 4 SPECTRIN REPEATS.
CC   -!- SIMILARITY: BELONGS TO THE PLAKIN OR CYTOLINKER FAMILY.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; AF260753; AAF70372.1; -.
DR   HSSP; Q01082; 1BKR.
DR   InterPro; IPR001589; Actbind_actinin.
DR   InterPro; IPR001715; Calponin-like.
DR   InterPro; IPR001101; Plectin_repeat.
DR   InterPro; IPR002017; Spectrin.
DR   Pfam; PF00307; CH; 2.
DR   Pfam; PF00668; Plectin; 20.
DR   SMART; SM00033; CH; 2.
DR   SMART; SM00250; PLEC; 32.
DR   SMART; SM00150; SPEC; 4.
DR   PROSITE; PS00019; ACTININ_1; PARTIAL.
DR   PROSITE; PS00020; ACTININ_2; FALSE_NEG.
DR   PROSITE; PS50021; CH; 2.
KW   Coiled coil; Repeat; Structural protein; Cytoskeleton; Actin-binding;
KW   Phosphorylation.
FT   NON_TER         1        1
FT   DOMAIN         <1     1259       GLOBULAR 1.
FT   DOMAIN       1260     2544       CENTRAL FIBROUS ROD DOMAIN.
FT   DOMAIN       2545     4473       GLOBULAR 2.
```

```
DR   InterPro; IPR005326; S10_plectin.
DR   InterPro; IPR002017; Spectrin.
DR   Pfam; PF00307; CH; 2.
DR   Pfam; PF03501; S10_plectin; 1.
DR   PROSITE; PS00019; ACTININ_1; 1.
DR   PROSITE; PS00020; ACTININ_2; FALSE_NEG.
DR   PROSITE; PS50021; CH; 2.
KW   Repeat; Structural protein; Cytoskeleton; Actin-binding.
KW   Alternative splicing.
FT   DOMAIN        181     >964       GLOBULAR.
FT   DOMAIN        185      411       ACTIN-BINDING.
FT   DOMAIN        293               CH 1.
FT   DOMAIN        306      408       CH 2.
FT   REPEAT        653      727       SPECTRIN 1.
FT   REPEAT        748      832       SPECTRIN 2.
FT   REPEAT        845      938       SPECTRIN 3.
FT   VARSPLIC        1        5       MVAGM -> MKIVP (IN ISOFORM PLEC 1D AND
FT                                    ISOFORM PLEC-1D,2A).
FT   VARSPLIC        1       15       MVAGMLMPLDRLRAI -> MEFSRATQHFISSLK (IN
FT                                    ISOFORM PLEC-1E AND ISOFORM PLEC-1E,2A).
FT   VARSPLIC        1       28       MVAGMLMPLDRLRAIYEVLFREGVMVAK -> MAHLETSGP
FT                                    PPDEQDPIQAYHEVRHKYK (IN ISOFORM PLEC-1F).
FT   VARSPLIC        1       33       MVAGMLMPLDRLRAIYEVLFREGVMVAKKDRRP -> MNET
FT                                    VCPFKI<SPS4GSINTLSPLPGTSVT>TKTS (IN ISOFORM
FT                                    PLEC-1I).
FT   VARSPLIC        1       37       MVAGMLMPLDRLRAIYFVLFREGVMVAKKDRRPRSLII ->
FT                                    MSQHRLRVPEPGLGSKRTSEDNLYLAVLRASECKK (IN
FT                                    ISOFORM PLEC-1A)
FT   VARSPLIC        1       37       MVAGMLMPLDRLRAIYEVLFREGVMVAKKDRRPRSLII ->
FT                                    MEPSGSLFPSLVVVGHVVTLAAVWIWRKGHRQAKDEQ (IN
FT                                    ISOFORM PLEC-1B AND ISOFORM PLEC-1B,2A)
FT   VARSPLIC        1       44       MVAGMLMPLDRLRAIYEVLFREGVMVAKKDRRPRSLIIPHIVP
FT                                    GVT -> MAGTWAAKGVFTSQREVILERPCWLDGCEQVRR
FT                                    GYLYGQLCCV (IN ISOFORM PLEC-1C).
FT   VARSPLIC        1       66       MVAGMLMPLDRLRAIYEVLFREGVMVAKKDRRPRSIHPHVP
FT                                    GVTNLQVMRAMASLKARGLVRETFA -> MSGEDSEVRPVA
FT                                    VAEGSSNGSSGSPSPGDTLPWNLGKTQPSPRSGGSVGNGS.
FT                                    VLDPAEPAVIPLA (IN ISOFORM PLEC-0,1C,
FT                                    ISOFORM PLEC-0,1C,2A,3A AND ISOFORM PLEC-
FT                                    0,1C,2A).
FT   VARSPLIC        1      242       MISSING (IN ISOFORM PLEC 1H).
FT   VARSPLIC        6      180       MISSING (IN ISOFORM PLEC-1D AND ISOFORM
FT                                    PLEC-1D,2A).
FT   VARSPLIC       16      180       MISSING (IN ISOFORM PLEC-1E).
FT   VARSPLIC       29      180       MISSING (IN ISOFORM PLEC-1F).
FT   VARSPLIC       34      180       MISSING (IN ISOFORM PLEC-1I).
FT   VARSPLIC       38      180       MISSING (IN ISOFORM PLEC-1A, ISOFORM
FT                                    PLEC-1B AND ISOFORM PLEC-1B,2A).
FT   VARSPLIC       45      180       MISSING (IN ISOFORM PLEC-1G).
FT   VARSPLIC       67      180       MISSING (IN ISOFORM PLEC-1C AND ISOFORM
FT                                    PLEC-0,1C,2A,3A).
FT   VARSPLIC      202      206       MISSING (IN ISOFORM PLEC 1, ISOFORM PLEC-
FT                                    1A, ISOFORM PLEC-1B, ISOFORM PLEC-1D,
FT                                    ISOFORM PLEC-1E, ISOFORM PLEC-1G, ISOFORM
FT                                    PLEC-1F, ISOFORM PLEC-0,1C AND ISOFORM PLEC
FT                                    PLEC-1B).
FT   VARSPLIC      239      239       E -> ERRVIRSVRLIRE (IN ISOFORM PLEC
FT                                    0,1C,2A,3A).
FT   CONFLICT      202      206       MISSING (IN REF. 2).
FT   NON_TER       964      964
SQ   SEQUENCE   964 AA;  111661 MW;  1E2846BF2B72AA3E CRC64;
```

```
Query Match            63.6%;  Score 35;  DB 1;  Length 964;
Host Local Similarity  63.6%;  Prod. No. 65;
Matches    7;  Conservative    1;  Mismatches    3;  Indels   0;  Gaps   0;

Qy      1 ELMLRLQDYEE 11
            | ||||||| ||
Db    424 ELQLRWQEYRE 434
```

```
RESULT 12
PLE1_CRIGR
```

```
FT   DOMAIN      -1     192   ACTIN-BINDING.
FT   DOMAIN      -1      74   CH 1.
FT   DOMAIN      87     189   CH 2.
FT   REPEAT     449     508   SPECTRIN 1.
FT   REPEAT     529     613   SPECTRIN 2.
FT   REPEAT     626     714   SPECTRIN 3.
FT   REPEAT    1104    1204   SPECTRIN 4.
FT   DOMAIN    1258    2548   COILED COIL (POTENTIAL).
FT   REPEAT    2615    2652   PLECTIN 1.
FT   REPEAT    2653    2690   PLECTIN 2.
FT   REPEAT    2691    2728   PLECTIN 3.
FT   REPEAT    2729    2766   PLECTIN 4.
FT   REPEAT    2770    2804   PLECTIN 5.
FT   REPEAT    2905    2942   PLECTIN 6.
FT   REPEAT    2943    2980   PLECTIN 7.
FT   REPEAT    2981    3018   PLECTIN 8.
FT   REPEAT    3019    3056   PLECTIN 9.
FT   REPEAT    3057    3094   PLECTIN 10.
FT   REPEAT    3274    3311   PLECTIN 11.
FT   REPEAT    3312    3349   PLECTIN 12.
FT   REPEAT    3350    3387   PLECTIN 13.
FT   REPEAT    3488    3425   PLECTIN 14.
FT   REPEAT    3429    3463   PLECTIN 15.
FT   REPEAT    3609    3646   PLECTIN 16.
FT   REPEAT    3647    3684   PLECTIN 17.
FT   REPEAT    3685    3722   PLECTIN 18.
FT   REPEAT    3723    3760   PLECTIN 19.
FT   REPEAT    3764    3797   PLECTIN 20.
FT   REPEAT    3800    3844   PLECTIN 21.
FT   REPEAT    3852    3889   PLECTIN 22.
FT   REPEAT    3890    3927   PLECTIN 23.
FT   REPEAT    3928    3965   PLECTIN 24.
FT   REPEAT    3966    4003   PLECTIN 25.
FT   REPEAT    4007    4041   PLECTIN 26.
FT   REPEAT    4043    4094   PLECTIN 27.
FT   REPEAT    4147    4234   PLECTIN 28.
FT   REPEAT    4235    4272   PLECTIN 29.
FT   REPEAT    4273    4310   PLECTIN 30.
FT   REPEAT    4311    4348   PLECTIN 31.
FT   REPEAT    4349    4386   PLECTIN 32.
FT   DOMAIN    4039    4089   BINDING TO INTERMEDIATE FILAMENTS (BY
FT                           SIMILARITY).
FT   DOMAIN    4414    4429   4 X 4 AA TANDEM REPEATS OF G-S-R-X.
FT   MOD_RES   4428    4428   PHOSPHORYLATION (BY CDC2).
SQ   SEQUENCE  4473 AA;  509015 MW;  E144615D361E3484 CRC64;
```

```
Query Match          63.6%;    Score 35;    DB 1;    Length 4473.
Best Local Similarity 63.6%;    Prod. No. 3.6e-02;
Matches  7;  Conservative 1;  Mismatches 3;  Indels 0,  Gaps 0;

Qy      1 ELMLKLQLYEE 11
            |  | ||: | | |
Db    205 ELQJLRWQEYRE 215
```

```
RESULT 13
ID   PLE1_HUMAN     STANDARD;         PRT;    4684 AA.
AC   Q15149; Q16640; Q15148;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, last sequence update)
DT   16-OCT-2001 (Rel. 40, last annotation update)
DE   Plectin 1 (PLTN) (PCN) (Hemidesmosomal protein 1) (HD1).
GN   PLEC1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   TISSUE=Placenta;
RX   MEDLINE=96210632; PubMed=8633055;
RA   Liu C.-G., Maercker C., Castanon M.J., Hauptmann R., Wiche G.;
```

RT   "Human plectin: organization of the gene, sequence analysis, and
RT   chromosome localization (8q24).";
RL   Proc. Natl. Acad. Sci. U.S.A. 93:4278-4283(1996).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORMS 2 AND 3), AND DISEASE.
RX   MEDLINE=96312447; PubMed=8698233;
RA   McLean W.H.I., Pulkkinen L., Smith F.J.D., Rugg E.L., Lane E.B.,
RA   Bullrich F., Burgeson R.E., Amano S., Hudson D.L., Owaribe K.,
RA   McGrath J.A., McMillan J.R., Eady R.A.J., Leigh I.M., Christiano A.M.,
RA   Uitto J.;
RT   "Loss of plectin causes epidermolysis bullosa with muscular dystrophy:
RT   cDNA cloning and genomic organization.";
RL   Genes Dev. 10:1724-1735(1996).
RN   [3]
RP   VARIANT MD-EBS 1003-GLN - ALA-1005 DEL.
RX   MEDLINE=97049959; PubMed=8894687;
RA   Pulkkinen L., Smith F.J.D., Shimizu H., Murata S., Yaoita H.,
RA   Hachisuka H., Nishikawa T., McLean W.H.I., Uitto J.;
RT   "Homozygous deletion mutations in the plectin gene (PLEC1) in patients
RT   with epidermolysis bullosa simplex associated with late onset
RT   muscular dystrophy.";
RL   Hum. Mol. Genet. 5:1539-1546(1996).
RN   [4]
RP   VARIANT MD-EBS LEU-429 INS.
RX   MEDLINE=21090821; PubMed=11159198;
RA   Bauer J.W., Rouan F., Kofler B., Reznizcek G.A., Kornacker I.,
RA   Muss W., Hametner R., Klausegger A., Huber A., Pohla-Gubo G.,
RA   Wiche G., Uitto J., Hintner H.;
RT   "A compound heterozygous one amino-acid insertion/nonsense mutation in
RT   the plectin gene causes epidermolysis bullosa simplex with plectin
RT   deficiency.";
RL   Am. J. Pathol. 158:617-625(2001).
```
CC   -!- FUNCTION: INTERLINKS INTERMEDIATE FILAMENTS WITH MICROTUBULES AND
CC       MICROFILAMENTS AND ANCHORS INTERMEDIATE FILAMENTS TO DESMOSOMES OR
CC       HEMIDESMOSOMES. COULD ALSO BIND MUSCLE PROTEINS SUCH AS ACTIN TO
CC       MEMBRANE COMPLEXES IN MUSCLE. MAY BE INVOLVED NOT ONLY IN THE
CC       CROSSLINKING AND STABILIZATION OF CYTOSKELETAL INTERMEDIATE
CC       FILAMENTS NETWORK, BUT ALSO IN THE REGULATION OF THEIR DYNAMICS.
CC   -!- SUBUNIT: HOMODIMER OR HOMOTETRAMER.
CC   -!- ALTERNATIVE PRODUCTS: 3 ISOFORMS; 1 (SHOWN HERE), 2 AND 3; ARE
CC       PRODUCED BY ALTERNATIVE SPLICING.
CC   -!- TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGHEST LEVELS IN
CC       MUSCLE, HEART, PLACENTA AND SPINAL CORD.
CC   -!- DOMAIN: THE N-TERMINUS INTERACTS WITH ACTIN, THE C-TERMINUS WITH
CC       VIMENTIN, DESMIN, GFAP, CYTOKERATINS, LAMIN B; WHEREAS BOTH THE N-
CC       AND THE C-TERMINUS CAN BIND INTEGRIN BETA-4.
CC   -!- PTM: PHOSPHORYLATED BY CDC2; REGULATES DISSOCIATION FROM
CC       INTERMEDIATE FILAMENTS DURING MITOSIS (BY SIMILARITY).
CC   -!- DISEASE: DEFECTS IN PLEC1 ARE THE CAUSE OF EPIDERMOLYSIS BULLOSA
CC       WITH MUSCULAR DYSTROPHY (MD-EBS OR EH-MD), AN AUTOSOMAL RECESSIVE
CC       DISORDER CHARACTERIZED BY EPIDERMAL BLISTER FORMATION AT THE LEVEL
CC       OF THE HEMIDESMOSOME AND ASSOCIATED LATE-ONSET MUSCULAR DYSTROPHY.
CC   -!- SIMILARITY: CONTAINS 1 ACTIN-BINDING DOMAIN.
CC   -!- SIMILARITY: CONTAINS 2 CALPONIN-HOMOLOGY (CH) DOMAINS.
CC   -!- SIMILARITY: CONTAINS 33 PLECTIN REPEATS.
CC   -!- SIMILARITY: CONTAINS 4 SPECTRIN REPEATS.
CC   -!- SIMILARITY: BELONGS TO THE PLAKIN OR CYTOLINKER FAMILY.
```

```
DR   EMBL; Z54367; CAA91196.1; -.
DR   EMBL; U53204; AAB05427.1; -.
DR   EMBL; U64610; AAB05428.1; -.
DR   EMBL; U64609; AAB05428.1; JOINED.
DR   EMBL; X97053; CAA65765.1; -.
DR   HSSP; Q01082; 1HKR.
DR   Genew; HGNC:9069; PLEC1.
```

```
DR   MIM; 601282;
DR   MIM; 226670;
DR   InterPro; IPR001589; Actbind_actinin.
DR   InterPro; IPR001715; Calponin-like.
DR   InterPro; IPR001101; Plectin_repeat.
DR   InterPro; IPR005326; S10_plectin.
DR   InterPro; IPR002017; Spectrin.
DR   Pfam; PF00307; CH; 2.
DR   Pfam; PF00681; Plectin; 19.
DR   Pfam; PF03501; S10_plectin; 1.
DR   SMART; SM00033; CH; 2.
DR   SMART; SM00250; PLEC; 33.
DR   SMART; SM00150; SPEC; 5.
DR   PROSITE; PS00019; ACTININ_1; FALSE_NEG.
DR   PROSITE; PS00020; ACTININ_2; FALSE_NEG.
DR   PROSITE; PS50021; CH; 2.
KW   Coiled coil; Repeat; Structural protein; Cytoskeleton; Actin-binding;
KW   Phosphorylation; Alternative splicing; Epidermolysis bullosa;
KW   Disease mutation.
FT   DOMAIN        1   1470       GLOBULAR 1
FT   DOMAIN     1471   2755       CENTRAL FIBROUS ROD DOMAIN
FT   DOMAIN     2756   4684       GLOBULAR 2.
FT   DOMAIN      175    400       ACTIN-BINDING.
FT   DOMAIN      179    282       CH 1.
FT   DOMAIN      295    397       CH 2.
FT   REPEAT      645    710       SPECTRIN 1
FT   REPEAT      740    824       SPECTRIN 2
FT   REPEAT      837    930       SPECTRIN 3
FT   REPEAT     1315   1415       SPECTRIN 4.
FT   DOMAIN     1469   2756       COILED COIL (POTENTIAL).
FT   REPEAT     2826   2863       PLECTIN 1.
FT   REPEAT     2864   2901       PLECTIN 2.
FT   REPEAT     2902   2939       PLECTIN 3.
FT   REPEAT     2940   2977       PLECTIN 4.
FT   REPEAT     2981   3015       PLECTIN 5.
FT   REPEAT     3116   3153       PLECTIN 6.
FT   REPEAT     3154   3191       PLECTIN 7.
FT   REPEAT     3192   3229       PLECTIN 8.
FT   REPEAT     3230   3267       PLECTIN 9.
FT   REPEAT     3268   3305       PLECTIN 10.
FT   REPEAT     3306   3343       PLECTIN 11.
FT   REPEAT     3485   3522       PLECTIN 12.
FT   REPEAT     3523   3560       PLECTIN 13.
FT   REPEAT     3561   3598       PLECTIN 14.
FT   REPEAT     3599   3636       PLECTIN 15.
FT   REPEAT     3640   3674       PLECTIN 16.
FT   REPEAT     3820   3857       PLECTIN 17.
FT   REPEAT     3858   3895       PLECTIN 18.
FT   REPEAT     3896   3933       PLECTIN 19.
FT   REPEAT     3934   3971       PLECTIN 20.
FT   REPEAT     3975   4008       PLECTIN 21.
FT   REPEAT     4063   4100       PLECTIN 22.
FT   REPEAT     4101   4138       PLECTIN 23.
FT   REPEAT     4139   4176       PLECTIN 24.
FT   REPEAT     4177   4214       PLECTIN 25.
FT   REPEAT     4218   4252       PLECTIN 26.
FT   REPEAT     4265   4305       PLECTIN 27.
FT   REPEAT     4319   4356       PLECTIN 28.
FT   REPEAT     4408   4445       PLECTIN 29.
FT   REPEAT     4446   4483       PLECTIN 30.
FT   REPEAT     4484   4521       PLECTIN 31.
FT   REPEAT     4522   4559       PLECTIN 32.
FT   REPEAT     4560   4597       PLECTIN 33.
FT   DOMAIN     4250   4300       BINDING TO INTERMEDIATE FILAMENTS (HY
FT                                SIMILARITY).
FT   DOMAIN     4625   4640       4 X 4 AA TANDEM REPEATS OF G-S-P-X.
FT   MOD_RES    4534   4534       PHOSPHORYLATION (BY CDC2) (BY
FT                                SIMILARITY).
FT   VARSPLIC      1    174       MVACMLMPRDQLRAIYEVLFREGVMVAKKDRRPRSLHPHVP
FT                                CVTNLQVMRAMASIRARGLVRETFAWCHFFWYLINKGIAHL
FT                                RQYLHLPPEIVAASIQRVRRPVAMVMPARRTPHVQAVQGPL
FT                                GSPPKRGPIPTEEQPLYPPKELEEVSPETPVVPATTQRTLA
FT                                RPAPEPAPAT -> MSGFTDAEVPAVSELVSNASSGSPSPGD
FT                                TLEWNLGKTQKSRHSGGSGASSNSVLLPAERAVIRTA (IN
FT                                ISOFORM 2 AND ISOFORM 3).
FT   VARSPLIC    499    412       MISSING (IN ISOFORM 3).
FT   VAR_ANT     429    429       L -> LL (IN MD-EBS).
FT                                /FTId=VAR_011336.
FT   VARIANT    1003   1005       MISSING (IN MD-EBS).
FT                                /FTId=VAR_011337.
FT   CONFLICT    185    185       S -> F (IN REF. 2).
FT   CONFLICT    259    259       N -> D (IN REF. 2).
FT   CONFLICT    550    550       H -> N (IN REF. 2).
FT   CONFLICT    550    550       I -> V (IN REF. 2).
FT   CONFLICT    706    706       Q -> R (IN REF. 2).
FT   CONFLICT    886    886       N -> Y (IN REF. 2).
FT   CONFLICT   1002   1002       V -> A (IN REF. 2).
FT   CONFLICT   1309   1309       V -> L (IN REF. 2).
FT   CONFLICT   1321   1321       L -> V (IN REF. 2).
FT   CONFLICT   1534   1534       V -> M (IN REF. 2).
FT   CONFLICT   1534   1534       I -> M (IN REF. 2).
FT   CONFLICT   1662   1662       A -> T (IN REF. 2).
FT   CONFLICT   1690   1690       WLG -> RLP (IN REF. 2).
FT   CONFLICT   1767   1767       Q -> E (IN REF. 2).
FT   CONFLICT   1789   1789       L -> A (IN REF. 2).
FT   CONFLICT   1910   1910       K -> R (IN REF. 2).
FT   CONFLICT   2154   2154       K -> N (IN REF. 2).
FT   CONFLICT   2160   2160       S -> R (IN REF. 2).
FT   CONFLICT   2215   2215       R -> Q (IN REF. 2).
FT   CONFLICT   2244   2244       S -> A (IN REF. 2).
FT   CONFLICT   3927   3927       K -> E (IN REF. 2).
FT   CONFLICT   3310   3310       E -> A (IN REF. 2).
FT   CONFLICT   3361   3361       F -> L (IN REF. 2).
FT   CONFLICT   3408   3408       F -> A (IN REF. 2).
FT   CONFLICT   3447   3447       S -> A (IN REF. 2).
FT   CONFLICT   3531   3531       G -> A (IN REF. 2).
FT   CONFLICT   3580   3580       R -> S (IN REF. 2).
FT   CONFLICT   3584   3584       S -> Q (IN REF. 2).
FT   CONFLICT   3596   3596       E -> Q (IN REF. 2).
FT   CONFLICT   3616   3616       N -> H (IN REF. 2).
FT   CONFLICT   3586   3586       V -> A (IN REF. 2).
```

```
Query Match             63.6%;   Score 35;  DB 1;  Length 4684;
Host Local Similarity   63.6%;   Pred. No. 3.8e-02;
Matches     7;  Conservative  1;  Mismatches  3;  Indels  0;  Gaps  0;

Qy         1 ELMLRLQDYEE 11
             |||||||||:||
Db       413 EIQIPWQPYPE 423
```

```
RESULT 14
PLE1_RAT
ID   PLE1_RAT      STANDARD;      PRT;   4687 AA.
AC   P30427; O08879; O08880; O08881;
DT   01-APR-1993 (Rel. 25, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Plectin 1 (PLTN) (PCN).
GN   PLEC1.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Murinae; Muridae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   TISSUE=Glial tumor;
RX   MEDLINE=91268156; PubMed=2050743;
RA   Wiche G., Becker B., Luber K., Weitzer G., Castanon M.J.,
RA   Hauptmann R., Stratowa C., Stewart M.;
RT   "Cloning and sequencing of rat plectin indicates a 466-kD polypeptide
RT   chain with a three-domain structure based on a central alpha-helical
RT   coiled coil.";
RL   J. Cell Biol. 114:83-99(1991).
RN   [2]
RP   REVISIONS.
```

```
RC   TISSUE=Glial tumor;
RX   MEDLINE=94210642; PubMed=8404055;
RA   Liu C.-G., Maercker C., Castanon M.J., Hauptmann R., Wiche G.;
RT   "Human plectin: organization of the gene, sequence analysis, and
RT   chromosome localization (8q24).";
RL   Proc. Natl. Acad. Sci. U.S.A. 93:4278-4283(1996).
RN   [4]
RP   PARTIAL SEQUENCE FROM N.A. (ISOFORMS 2, 3, 4), AND TISSUE SPECIFICITY
RC   TISSUE=Glial tumor;
RX   MEDLINE=97421050; PubMed=9177781;
RA   Elliott C.E., Becker B., Oehler S., Castanon M.J., Hauptmann R.,
RA   Wiche G.;
RT   "Plectin transcript diversity: identification and tissue distribution
RT   of variants with distinct first coding exons and rodless isoforms.";
RL   Genomics 42:115-125(1997).
CC   -!- FUNCTION: INTERLINKS INTERMEDIATE FILAMENTS WITH MICROTUBULES AND
CC       MICROFILAMENTS AND ANCHORS INTERMEDIATE FILAMENTS TO DESMOSOMES OR
CC       HEMIDESMOSOMES. MAY BE INVOLVED NOT ONLY IN THE CROSSLINKING AND
CC       STABILIZATION OF CYTOSKELETAL INTERMEDIATE FILAMENTS NETWORK, BUT
CC       ALSO IN THE REGULATION OF THEIR DYNAMICS.
CC   -!- SUBUNIT: HOMODIMER OR HOMOTETRAMER.
CC   -!- ALTERNATIVE PRODUCTS: 4 ISOFORMS: 1 (SHOWN HERE), 2, 3 AND 4; ARE
CC       PRODUCED BY ALTERNATIVE SPLICING.
CC   -!- TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGHEST EXPRESSION IN
CC       SKELETAL MUSCLE AND LOWEST IN THYMUS
CC   -!- DOMAIN: THE N-TERMINUS INTERACTS WITH ACTIN, THE C-TERMINUS WITH
CC       VIMENTIN, DESMIN, GFAP, CYTOKERATINS, LAMIN B; WHEREAS BOTH THE N-
CC       AND THE C-TERMINUS CAN BIND INTEGRIN BETA-4.
CC   -!- PTM: PHOSPHORYLATED BY CDC2; REGULATES DISSOCIATION FROM
CC       INTERMEDIATE FILAMENTS DURING MITOSIS (BY SIMILARITY).
CC   -!- SIMILARITY: CONTAINS 1 ACTIN-BINDING DOMAIN.
CC   -!- SIMILARITY: CONTAINS 2 CALPONIN-HOMOLOGY (CH) DOMAINS.
CC   -!- SIMILARITY: CONTAINS 33 PLECTIN REPEATS.
CC   -!- SIMILARITY: CONTAINS 4 SPECTRIN REPEATS.
CC   -!- SIMILARITY: BELONGS TO THE PLAKIN OR CYTOLINKER FAMILY.
CC   -!- CAUTION: ISOFORM 4 IS A FRAGMENT AT THE N-TERMINUS
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; X59601; CAA42169.1; -.
DR   EMBL; U96274; AAC53209.1; -.
DR   EMBL; U96275; AAC53210.1; -.
DR   EMBL; U96276; AAC53211.1; -.
DR   PIR; A59648; A59638.
DR   PIR; S21876; S21876.
DR   HSSP; Q01082; 1HKR.
DR   InterPro; IPR001589; Actbind_actnin.
DR   InterPro; IPR001715; Calponin-like.
DR   InterPro; IPR001101; plectin_repeat.
DR   InterPro; IPR005326; S10_plectin.
DR   InterPro; IPR020017; Spectrin.
DR   Pfam; PF00307; CH; 2.
DR   Pfam; PF00681; Plectin; 21.
DR   Pfam; PF04501; S10_plectin; 1.
DR   SMART; SM00033; PLEC; 33.
DR   SMART; SM00150; SPEC; 4.
DR   PROSITE; PS00019; ACTININ_1; FALSE_NEG.
DR   PROSITE; PS00020; ACTININ_2; FALSE_NEG.
DR   PROSITE; PS50021; CH; 2.
KW   Coiled coil; Repeat; Structural protein; Cytoskeleton; Actin-binding;
KW   Phosphorylation; Alternative splicing.
FT   DOMAIN       181    288       CH 1.
FT   DOMAIN       301    403       CH 2.
FT   REPEAT       648    722       SPECTRIN 1.
FT   REPEAT       743    827       SPECTRIN 2.
FT   REPEAT       840    933       SPECTRIN 3.
FT   REPEAT      1318   1418       SPECTRIN 4.
FT   DOMAIN      1472   1692       COILED COIL (POTENTIAL).
FT   DOMAIN      1724   2760       COILED COIL (POTENTIAL).
FT   REPEAT      2791   2838       PLECTIN 1.
FT   REPEAT      2829   2866       PLECTIN 2.
FT   REPEAT      2867   2904       PLECTIN 3.
FT   REPEAT      2905   2942       PLECTIN 4.
FT   REPEAT      2943   2980       PLECTIN 5.
FT   REPEAT      2984   3018       PLECTIN 6.
FT   REPEAT      3119   3156       PLECTIN 7.
FT   REPEAT      3157   3194       PLECTIN 8.
FT   REPEAT      3195   3232       PLECTIN 9.
FT   REPEAT      3233   3270       PLECTIN 10.
FT   REPEAT      3271   3308       PLECTIN 11.
FT   REPEAT      3311   3346       PLECTIN 12.
FT   REPEAT      3488   3525       PLECTIN 13.
FT   REPEAT      3526   3563       PLECTIN 14.
FT   REPEAT      3564   3601       PLECTIN 15.
FT   REPEAT      3602   3639       PLECTIN 16.
FT   REPEAT      3643   3677       PLECTIN 17.
FT   REPEAT      3823   3860       PLECTIN 18.
FT   REPEAT      3861   3898       PLECTIN 19.
FT   REPEAT      3899   3946       PLECTIN 20.
FT   REPEAT      3937   3974       PLECTIN 21.
FT   REPEAT      3978   4011       PLECTIN 22.
FT   REPEAT      4066   4103       PLECTIN 23.
FT   REPEAT      4104   4141       PLECTIN 24.
FT   REPEAT      4142   4179       PLECTIN 25.
FT   REPEAT      4180   4217       PLECTIN 26.
FT   REPEAT      4221   4255       PLECTIN 27.
FT   REPEAT      4268   4308       PLECTIN 28.
FT   REPEAT      4411   4448       PLECTIN 29.
FT   REPEAT      4449   4486       PLECTIN 30.
FT   REPEAT      4487   4524       PLECTIN 31.
FT   REPEAT      4525   4562       PLECTIN 32.
FT   REPEAT      4563   4600       PLECTIN 33.
FT   DOMAIN      4253   4303       BINDING TO INTERMEDIATE FILAMENTS.
FT   DOMAIN      4628   4643       4 X 4 AA TANDEM REPEATS OF G-S-R-X.
FT   MOD_RES     4542   4542       PHOSPHORYLATION (BY CDC2) (BY
FT                                 SIMILARITY).
FT   VARSPLIC       1    180       MVAGMLMPLIDQLRAIYEVLFREGVMVAKKDRRPRSLHPHVP
FT                                 GVTNLQVMRAMTSLKARGLVRETFAWCHFYWYLTNEGIDHL
FT                                 RQYLHLPPEIVPASLQRVRRPVAMVMPARRKSPHVQIMGQP
FT                                 LGCPPKRGPLPAEDPAREEPQVYPPKEFEEGAPETPVVSAT
FT                                 IVGTLARPGPFPTPAT -> MSQQRLFVPEPEPGLGSKPTSS
FT                                 EDNLYLAVLRASEGKK (IN ISOFORM 2).
FT   VARSPLIC       1    180       MVAGMLMPLIDQLRAIYEVLFREGVMVAKKDRRPRSLHPHVP
FT                                 GVTNLQVMRAMTSLKARGLVRETFAWCHFYWYLTNEGIDHL
FT                                 RQYLHLPPEIVPASLQRVRRPVAMVMPARRKSPHVQIMGQP
FT                                 LGCPPKRGPLPAEDPAREERQVYRRKEREEGAPETPVVSAT
FT                                 IVGTLARPGPFPTPAT -> MEPSGSLFPSLVVVGHVVSLA
FT                                 AVWHWRKGHRQAQDEQ (IN ISOFORM 3).
FT   VARSPLIC       1    180       MVAGMLMPLIDQLRAIYEVLFREGVMVAKKDRRPRSLHPHVP
FT                                 GVTNLQVMRAMTSLKARGLVRETFAWCHFYWYLTNEGIDHL
FT                                 RQYLHLPPEIVPASLQRVRRPVAMVMPARRKSPHVQIMGQP
FT                                 LGCPPKRGPLPAEDPAREEPQVYRRKEREEGAPETPVVSAT
FT                                 IVGTLARPGPFPTPAT -> IVSN&SSGSPSPGDTLPWNLG
FT                                 KTQRSRRSGGGSVGNGSVLDPAERAVIRIA (IN
FT                                 ISOFORM 4).
SQ   SEQUENCE   4687 AA;  533527 MW;  9966CAF71H029751 CRC64;

Query Match             63.6%;  Score 45;  DB 1;  Length 4687;
Best Local Similarity   63.6%;  Pred. No. 3.8e+02;
Matches    7;  Conservative    1;  Mismatches   3;  Indels    0;  Gaps    0;

Qy          1 ELMRLRQDYEE 11
              ||| | | | |
Db        419 ELQLRWQEYRE 429
```

Db   196 ELLVDLQDYD 205

Search completed: January 16, 2003, 16.51.14
Job time : 17.0286 secs

RESULT 15
KC2A_MAIZE
ID   KC2A_MAIZE   STANDARD;   PRT;   332 AA.
AC   P28523;
DT   01-DEC-1992 (Rel. 24, Created)
DT   01-DEC-1992 (Rel. 24, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Casein kinase II, alpha chain (CK II) (EC 2.7.1.37) (CK2-alpha).
CN   ACK2.
OS   Zea mays (Maize).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC   Panicoideae; Andropogoneae; Zea.
OX   NCBI_TaxID=4577;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. B73 Inbred;
RX   MEDLINE=92096457; PubMed=1756176;
RA   Dobrowolska G., Boldyreff B., Issinger O.-G.;
RT   "Cloning and sequencing of the casein kinase 2 alpha subunit from Zea
RT   mays.";
RL   Biochim. Biophys. Acta 1129:139-140(1991).
RN   [2]
RP   X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS)
RX   MEDLINE=98232491; PubMed=9564028;
RA   Niefind K., Guerra B., Pinna L.A., Issinger O.G., Schomburg D.;
RT   "Crystal structure of the catalytic subunit of protein kinase CK2
RT   from Zea mays at 2.1-A resolution.";
RL   EMBO J. 17:2451-2462(1998).
CC   -!- FUNCTION: CASEIN KINASES ARE OPERATIONALLY DEFINED BY THEIR
CC   PREFERENTIAL UTILIZATION OF ACIDIC PROTEINS SUCH AS CASEINS
CC   AS SUBSTRATES. THE ALPHA CHAIN CONTAINS THE CATALYTIC SITE.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SUBUNIT: TETRAMER OF TWO ALPHA AND TWO BETA CHAINS (POSSIBLE).
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC   CK2 SUBFAMILY.
CC   --
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --
DR   EMBL; X61387; CAA43659.1; -.
DR   PIR; S16387; S16387.
DR   PIR; S19726; S19726.
DR   PDB; 1LP4; 29-MAY-02.
DR   MaizeDB; 30032; -.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   ProDom; PD000001; Euk_pkinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   Transferase; Serine/threonine-protein kinase; ATP-binding;
KW   3D-structure.
FT   DOMAIN   34   319   PROTEIN KINASE.
FT   NP_BIND   40   48   ATP.
FT   BINDING   63   63   ATP.
FT   ACT_SITE   151   151
SQ   SEQUENCE   332 AA; 39230 MW; 85513A5A5C77235A CRC64;

Query Match   61.8%; Score 34; DB 1; Length 332;
Best Local Similarity   60.0%; Pred. No. 31;
Matches   6; Conservative   3; Mismatches   3; Indels   0; Gaps   0;

Qy   1 ELMRLQDYE 10
           || :: |||:

Db   196 ELLVDLQDYD 205